

# BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

## AJ242652:Hepatitis C virus replicon I377/NS3-3'UTR

Results for: [emb|AJ242652.1](#) Hepatitis C virus replicon I377/NS3-3'UTR(7989bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

### Query ID

gi|5441834|emb|AJ242652.1|

### Description

Hepatitis C virus replicon I377/NS3-3'UTR

### Molecule type

nucleic acid

### Query Length

7989

### Subject ID

29035

### Description

None

### Molecule type

nucleic acid

### Subject Length

9599

### Program

BLASTN 2.2.21+ [Citation](#)

### Reference

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

## Search Parameters

Program	blastn
Word size	28
Expect value	10
Hitlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

## Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.33271	1.28
K	0.620991	0.46
H	1.12409	0.85

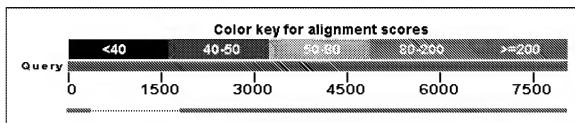
## Results Statistics

## Graphic Summary

## Distribution of 2 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



## Plot of gi|5441834|emb|AJ242652.1| vs 29035

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



### Descriptions

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

### Sequences producing significant alignments:

(Click headers to sort columns)

29035	4447	5111	82%	0.0	98%
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Alignments **Select All** Get selected sequences Distance tree of results Multiple alignment **NEW**

>1c1|29035  
Length=9599

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Score = 4447 bits (2408), Expect = 0.0  
Identities = 5058/6316 (80%), Gaps = 268/6316 (4%)  
Strand=Plus/Plus

Query	1802	TGGCGCCTATTACGGCCCTACTCCCAACAGACGCGAGGCCCTACTTGGCTGCATCACTACTA	1861
Sbjct	3418	TGGCGCCCATCAGCGCGTACGCCACAGACGAGAGGCCCTCCTAGGGTGTATAATCACCA	3477
Query	1862	GCCTCACAGCGCGGACAGGAACAGGTCGAGGGGGAGGTCCAAG-TGGTCTCCACCGCA	1920
Sbjct	3478	GCCTGACTGGCGGGACAAAAACCAAGTGGAGGGTGAAGTCC-AGATCGTGTCAACTGCT	3536
Query	1921	ACACAATCTTTCTTGGCGACCTGCGTCAATGGCGTGTGTGGACTGTCTATCATGGTGCC	1980
Sbjct	3537	ACCCAAACCTTCTTGGCAACGTGCATCAATGGGGTATGTCTGGACTGTCTACCAACGGGCGC	3596
Query	1981	GGCTCAAAGACCTTGCCGGC-CCAAAGGGCCCAATCACCACAAATGTACACCAATGTGGA	2039
Sbjct	3597	GGAACGAGGACCATCG-CATCACCACAGGGTCTGTGTATCCAGATGTATACCAATGTGGA	3655
Query	2040	CCAGGACCTCGTCGGCTGGCAAGCGCCCCCGGGGGCGCGTTCCTTGACACCATGCACCTG	2099
Sbjct	3656	CCAAGACCTTGTGGGCTGGCCCGCTCCTCAAGGTTCCCGCTCATTGACACCTGTACCTG	3715
Query	2100	CGGCAGCTCGGACCTTTACTTGGTCACGAGGCATGCCGATGTCTATCCGGTGCAGCGGCG	2159
Sbjct	3716	CGGCTCCTCGGACCTTTACTTGGTCACGAGGCACGCCGATGTCTATCCCGTGCAGCGGCG	3775
Query	2160	GGGCGACAGAGGGGGAGCCTACTCTC-CCCCAGGCCCGTCTCTACTTGAAGGGCTCTT	2218
Sbjct	3776	AGGTGATAGCAGGGGTAGCCTGCTTTGCGCCC-GGCCCATTTCTACTTGAAGGGCTCTT	3834
Query	2219	CGGGCGGTCCACTGTCTGTGCCCCCTCGGGGACGCTGTGGGCATCT-TTC-GGGCTGCCGT	2276
Sbjct	3835	CGGGGGTCCGCTGTGTGTGCCCCGCGGGACACGCGGTGGGC--TATTACAGGGCCGCGGT	3892
Query	2277	GTGCACCCGAGGGGTTGCGAAGGCGGTGGACTTTGTACCC-GTCGAG--TCTATGGAAC	2333
Sbjct	3893	GTGCACCCGTGGAGTGGCTAAAGCGGTGGACTTTAT-CCCTGTGGAGAACCTA-GG-GAC	3949
Query	2334	CACATGCGGTCCCCGGTCTTCACGGACAACCTCGTCCCCCTCGGGCCGTACCCGAGA-CAT	2392
Sbjct	3950	AACCATGAGATCCCCGGTGTTCACGGACAACCTCCTCTCCACACGACGTGCCCGAGAGC-T	4008
Query	2393	TCCAGGTGGCCCATCTACACGC-CCCTACTGGTAGCGGCAAGGACATAGGTGCCGGCT	2451
Sbjct	4009	TCCAGGTGGCCCACTTGCATGCTCCC-ACCGGCAGCGGTAAAGACCAAGTTCGGGCT	4067
Query	2452	GCGTATGACGCCCAAGGG-TATAAGGTGCTT-GTCTGAACCCGTCCGTGCGCGCCACCC	2509
Sbjct	4068	GCGTACGACGCC-AGGGCTACAAGGTG-TTGGTGTCAACCCCTCTGTGTGTGCAAGCG	4125
Query	2510	TAGG-TTTCGGGGCGTATATGTCTAAGGCACATGGTATCGACCCCTAACATCAGAACCGGG	2568
Sbjct	4126	TGGGCTTT-GGTGCTTACATGTCCAAGGCCATGGGGTGTATCTAATATCAGGACCGGG	4184
Query	2569	GTAAGGACCATCACAC-GGGTGCCCCCATCAGTACTCCACCTATGGCAAGTTTCTTGC	2627

Sbjct	4185	GTGAGAACAAATACCACTGGCAG-CCCATCACGTAACCTTACGGCAAGTTCCTTGC	4243
Query	2628	CGACGGTGGTTCCTCTGGGGGCGCCTATGACATCATAATATGTGATGAGTGGCCTCAAC	2687
Sbjct	4244	CGACGGCGGGTCTCAGGAGGTGCTTATGACATAAATAATTTGTGACGAGTGGCCTCCAC	4303
Query	2688	TGACTCGACCAC-T--ATCCTGGGCATCGGCACAGTCTTGGACCAAGCGGAGACGGCTGG	2744
Sbjct	4304	GGA-T-G-CCACATCCATCTTGGGCATCGGCACGTGCTTGGACCAAGCAGAGACTGCGGG	4360
Query	2745	AGCGGCACTCGTGTGCTCGCCACCGCTACGGCTCCGGGATCGTTCACCGTG-CCACATC	2803
Sbjct	4361	GGCGAGACTGGTGTGCTCGCCACTGCTACCCCTCCGGGCTCCGTCACTGTGTCC-CATC	4419
Query	2804	CAACATCGAGGAGGTGGCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAAGCCA	2863
Sbjct	4420	CTAACATCGAGGAGGTGGCTCTGTCCACCACCGGAGAGATCCCTTTTACGGCAAGGCTA	4479
Query	2864	TCCCATTCGAGACCATCAA <del>gggggg</del> AGGCACCTCATTTTCTGCCATTCCAAGAGAAAT	2923
Sbjct	4480	TCCCTCTCGAGGTGATCAAGGGGGGAAGACATCTCATCTTCTGCCACTCAAAGAAGAACT	4539
Query	2924	GTGATGAGCTCGCCGGCAAGCT-CTCCGGCTCGGAG-TCAAATGCTGTAGCATATTACCG	2981
Sbjct	4540	GGCAGCAGTCTCGCCGGCAAGCTGGT-C-GCATTGGGCATCAATGCCGTGGCTACTACCG	4597
Query	2982	GGGCTTGATGATATCCGTATACCAACTAGCGGAGACCTCATTGTCGTAG-CAACGGACG	3040
Sbjct	4598	CGGTCTTGACGTGTGTCTCATCCGACACGCGGCGATGTTGTCTGTGT-GTCGACCGATG	4656
Query	3041	CTCTAATGACGGGCTTTACGGCGGATTTGCACTCAGTGATCGACTGCAATACATGTGTCA	3100
Sbjct	4657	CTCTCATGACTGGCTTTACGGCGGACTTCGACTCTGTGATAGACTGCAACACGCTGTGTCA	4716
Query	3101	CCCAGACAGTCGACTTCAGCCTGGACCCGACCTTCACCATTTGAGACGACGACCG-TGCCA	3159
Sbjct	4717	CTCAGACAGTCGATTTAGCCTTGACCTTACCTTTACCATTTGAGACACCA-CGTCCCC	4775
Query	3160	CAAGACCGGGTGT-CAGCTCGCAGCGGCGAGGACGAGTGGTAGGGGACGATGGGCAT	3218
Sbjct	4776	CAGGATGCTGTCTCCA-GGACTCAACCGCGGGGACGAGTGGCAGGGGGAAGCCAGGCAT	4834
Query	3219	TTACAGGTTTGTGACTCCAGGAGAACCGGCCCTCGGGCATGTTTCGATTTCCTCGGTTCTGTG	3278
Sbjct	4835	CTATAGATTTGTGGACCGGGGGAGCGCCCTCCGGCATGTTTCGACTCGTCCGTCTCTGTG	4894
Query	3279	CGAGTGTCTATGACGCGGGCTGTGCTTGGTACGAGCTCAGCCCGCCGAGACCT-CAGTTA	3337
Sbjct	4895	TGAGTGTCTATGACGCGGGCTGTGCTTGGTATGAGCTCAGCCCGCCGAGAC-TACAGTTA	4953
Query	3338	GGTTGGGGGCTTACCTAAACACACAGGG-TTGGCGGTGTGCCAGGACCATCTGGAGTTC	3396
Sbjct	4954	GGCTACGAGCGTACATGAACACCCCGGGGCTT-CCGCTGTGCCAGGACCATCTTGAATTT	5012
Query	3397	TGGGAGAGCGTCTTTACAGGCCTCACCCACATAGACGCCCA-TTCTTGTCCGAGACTAA	3455
Sbjct	5013	TGGGAGGGCGCTTTTACGGGCTTCACTCATATAGATGCCACCTTT-TTATCCGACACAAA	5071
Query	3456	GCAG-GCAGGAGACAACCTTCCCCTACCTGGTAGCATACCAGGCTACGGTGTGCGCCAGGG	3514
Sbjct	5072	GCAGAGTGGG-GAGAACTTCCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCTAGGG	5130
Query	3515	CTCAGGCTCCACCTCCATCGTGGGACAAATGTGGAAGTGTCTCATACGGCT-AAAGCCT	3573
Sbjct	5131	CTCAAGCCCTTCCCTCATCGTGGGACAGATGTGGAAGTGTTCATCCGCTTAAACCC-	5189
Query	3574	ACGCTGCACGGGCAACGCCCTTGTGTATAGGCTGGGAGCGCTTCAAACGAGGTACT	3633
Sbjct	5190	ACCTTCCATGGGCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAAATGAATCAC-	5248
Query	3634	ACC--ACACACCCCATAAACAAATACATCATGGGCATGCATGTGGCTGACCTGGAGGTCG	3691
Sbjct	5249	-CCTGAGCGCACCAATACCAAAATACATCATGACATGCATGTGGCGGACCTGGAGGTCG	5307
Query	3692	TCACGAGCACCTGGGTGCTGGTAGGCGGAGTCCTAGCAGCTCTGGCGCGGATTTGCCGTGA	3751
Sbjct	5308	TCACGAGCACCTGGGTGCTGGTAGGCGGAGTCCTAGCAGCTCTGGCGCGGATTTGCCGTGA	5367
Query	3752	CAACAGGCAAGCTGGTCACTTGGGGCAGGATCATCTTGTGCCGGAAGCCGGGCATCATTC	3811
Sbjct	5368	CAACAGGCTGCGTGGTCACTAGTGGGCAGGATCGTCTTGTCCGGGAAGCCGGCAATATATC	5427

Query 3812 CCGACAGGGGAAGTCTCTTACCGGGAGTTCGATGAGATGGAAGAGTGGCGCTCA-CACCTC 3870

Sbjct 5428 CTGACAGGGAGGTTCTCTACCAGGAGTTCGATGAGATGGAAGAGTGGCTC-TCAGCACTTA 5486

Query 3871 CCTTACATCGAACA-GGGAATGCA-GCTCGCCGAACAATTCAAACAGAAGGCAATCGGGT 3928

Sbjct 5487 CCGTACATCAGGCAACGGGA-TG-ATGCTCGCTGAGCAGTTCAACAGAGAAGGCCCTCGGCC 5544

Query 3929 TCGTGCACAAACAGCCCAAGCAA-GCGGAGGCTGCTGCTCCCGTGGTGG--A-ATCCAAAG 3984

Sbjct 5545 TCGTGCAGACCGCGTCCC-GCCATGCAGAGTTA-T-CACCCCTGCTGTCCAGA-CCAAAC 5600

Query 3985 TGGCGGACCCCTCGAAGCCCTCTGGGCGAAGCATATGTGGAATTTTCATCAGCGGGATACAA 4044

Sbjct 5601 TGGCAGAAATCGAGGTCTTTTGGGCGAAGACATGTGGAATTTTCATCAGTGGGATACAA 5660

Query 4045 TATTTAGCAGGCTTGTCCTCTGCCCTGGCAACCCCGCATAGCATCAGTATGGCATTTC 4104

Sbjct 5661 TACTTGGCGGGCTGTCAACGCTGCCCTGGTAACCCCGCATTTGCTTCATGATGGCTTTT 5720

Query 4105 ACAGCCT-CTATCACCAGCCGCTCACCACCAACATACCCCTCTGTTTAAACATCCTGGG 4163

Sbjct 5721 ACAGC-TGCCGTACACCAGCCCACTAACCATGGCCAAACCCCTCTCTTCAACATATTGGG 5779

Query 4164 GGGATGGGTGGCGGCCCAACTTGCT-CTTCCACGCGCTGCTTCTGCG-TTTGCTAGGCGGCC 4221

Sbjct 5780 GGGGTGGGTGGTGCACAGCTCGCCGCC-CCCGGTGCCGCTACTGCCCTT-TGGGGTGCT 5837

Query 4222 GGCACTCGCTGGAGCGGCTGTGGCAGCATAGGCCCTGGGAAGGTGCTTGTGGATATT-TT 4280

Sbjct 5838 GGCCTAGCTGGCGCCGCCATCGGCAGCGTTGGACTGGGAAGGTCTCTGTGGACATTCCT 5897

Query 4281 GGCAGGTTATGGAGCAGGG-GTGGCAGCGCGCTCGTGGCCCTTAAAGTTCATGAGCGGCG 4339

Sbjct 5898 G-CAGGCTTCCGCGC-GGGCGTGGCGGAGCTCTTGTAGCATCTCAAGTATCATGAGCGGCTG 5955

Query 4340 AGATGCCCTCAGCGAGGACCTGGTTAACCTACT-CCCTGCTATCCCTCTCCCTCGGCGGCC 4398

Sbjct 5956 AGGTCCCTCCACGAGGAGCTGGTCAATCTGCTGGCC-GCCATCCTCTCGCTGGAGCC 6014

Query 4399 CTAGTCTGTCGGGGTCTGTGCGCAGCGATCTGCGCTCGGCACGTGGGCCACAGG-GAGGG 4457

Sbjct 6015 CTTGTAGTCTGGTGTGCTGCGCAGCAATCTGCGCCGACGCTGGGCC-GGGCGAGGG 6073

Query 4458 GGCTGTGCACTGGATGAACCGGCTGATAGCGTTTCGCTTCGCGGGGTAAACAGCTCTCCCC 4517

Sbjct 6074 GGCAGTGCAATGGATGAACCGGCTAATAGCCTTCGCCCTCCGGGGGAACCATGTTTCCCC 6133

Query 4518 CACGCACTATGTGCTGAGAGCGACGCTGCAGCACGTGTCACT-CAGATCCTCT-CTAGT 4575

Sbjct 6134 CACGCACTACGTGCCGAGAGCGATGCAGCGCCCGCGCTCACTGCC-ATACTCAGC-AGC 6191

Query 4576 CTTACCATCACTCAGCTGCTGAAGAGGCTTCACGAGTGGATCAA-CGAGGACTGCT-CCA 4633

Sbjct 6192 CTCAGTCTAACCCAGCTCCTGAGGCGACTGCATCAGTGGAT-AAGCTCGGAGTG-TACCA 6249

Query 4634 CGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTGGATATGC-ACGGTGTGA-C 4691

Sbjct 6250 CTCATGCTCCGGTTCCTGGCTAAGGGACATCTGGGACTGGATATGCGA-GGTGCTGAGC 6308

Query 4692 TGA-TTTCAAGACCTGGCTCCA-GTCCAAGCTCCTGCCGCGATTGGC-GGGAGTCCCCCTT 4748

Sbjct 6309 -GACTTT-AAGACCTGGCTGAAAG-CCAAGCTCATGCCAACACTGCCTGGGATTCCTTT 6365

Query 4749 CT-TCCTACTCAACGTGGGTACAAGGAGTCTGGCGGGGACGCGCATCATGCAAAAC-C 4806

Sbjct 6366 GTGCT-C-TGCCAGCGCGGGTATAGGGGGGTCTGGCGAGGAGACGGCATATGACACATC 6423

Query 4807 ACCTGCC-CATGTGGAGCACAGATCACCGACATGTGAAAAACGGTTCCATGAGGATCGT 4865

Sbjct 6424 GC-TGCCAC-TGTGGAGCTGAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGT 6481

Query 4866 GGGGCTAGGACCTGTAGTAACACGCTGGCA-TGGAACATTTCCCATTAACCGCTACACCA 4924

Sbjct 6482 CGGTCTTAGGACCTGCAGGAACATGTGG-AGTGGGACGTTCCCATTAACCGCTACACCA 6540

Query 4925 CGGGCCCCCTGCACGCC-TCGCCGCGCCAAATATTTC-TAGGGCGCTGTGGCGGGTGGC 4982

Sbjct 6541 CGGGCCCCCTGTACTCCCTTCCTG-CGCCGAACATAAGTTTCG-CGCTGTGGAGGGTGTG 6598

Query 4983 TGCTGAGGAGTACGTGGAGGTACGCGGGTGGGGGATTTCACACTACGTGA-CGGGCATGA 5041

Sbjct 6599 TGCAGAGGAATACGTGGAGATAAGGCGGGTGGGGGACTTCCACTACGT-ATCGGGTATGA 6657

Query 5042 CCACCTGACAA-CGTAAGTGGCCGTGTGAGGTTCCGGCCCCGGAATTTCTTCACAGAAGTG 5100

Sbjct 6658 CTACTGACAACTTAA--TGCCCGTGCCAGATCCCATCGCCCGAATTTTTCACAGAATTG 6716

Query 5101 GATGGGGTGGCGTTGCACAGGTACGCTCCAGCGTGCAAAACCCCTCCTACGGGAGGAGGTC 5160

Sbjct 6717 GACGGGGTGGCGCTACACAGGTTTGGGCCCTTGCAGCCCTTGCTGCGGGAGGAGGT- 6775

Query 5161 A-CATTCTGT-GTCCGGCTCAATCAA-TACCTGGTTGGGTACAGCTCCCATGCGAGGCC 5217

Sbjct 6776 ATCATTC-A-GATAGGACTCCA-CGAGTACCCGGTGGGTGCGAATTAACCTGCGAGGCC 6833

Query 5218 GAACCGGACGTAGCAGTGCTCACTTCCATGCTACCGACCCCTCCCACATTACGGCGGAG 5277

Sbjct 6834 GAACCGGACGTAGCCGTGTGAGCTCCATGCTCACTGATCCCTCCCATATAACACGACAG 6893

Query 5278 ACCGGCTAAGCGTAGGCTGGCCAG-GGGATCTCCCCCTCCT-TGGCCAGCTCATCAGCTA 5335

Sbjct 6894 GCGCGCCGGGAGAAGGTTGGCGAGAGGG-TCACCCCTTC-TATGGCCAGCTCCTCGGCTA 6951

Query 5336 GCCAGCTGTCTGGCGCTTC-CTTGAAGGCAACATGCATACCCGCTGACTCCCGGAC 5394

Sbjct 6952 GCCAGCTGTCTGGCTCCATCTCTC-AAGGCAACTTGACCGCCCAACCATGACTCCCTGAC 7010

Query 5395 GCTCAGCTCATCGAGGCCAACCTCCTGTGGCGGAGGAGATGGCGGGAACATCACCCGC 5454

Sbjct 7011 GCGGAGCTCATAGAGGCTAACCTCCTGTGGAGGAGGAGATGGCGGGAACATCACCAAG 7070

Query 5455 GTGGAGTCAGAAAATAAGGTAGTAATTTTGGACTCTTTGAGCGCCCTCCAGCGGAGGAG 5514

Sbjct 7071 GTTGAGTCAGAGAACAAGTGGTGATTCTGGACTCCTTGATGCTCGCTTGTGGCAGAGGAG 7130

Query 5515 GATGAGAGGGAAGTATCCGTTCCGGCGGAGATCCTGCGGAGGTC-CAGGAATTC-CCTC 5572

Sbjct 7131 GATGAGCGGGAGGTCCTCCGTACCTGCAGAAATCTGCGGAGCTCTC-GGAGATTCCGC-C 7188

Query 5573 GAGCGATGCCCATATGGGACGCGCCGGATTACAACCTCCACT-GTTAGAGTCTTGGAAAG 5631

Sbjct 7189 GGGCCCTGCCCTCTGGGCGGGCGGACTACAACCCCGCTAGT-AGAGAGCTGGAAA 7247

Query 5632 GACCCGGACTACGTCCCTCCAGTGGTACACGGGTGTCATTGCCGCCTGCCAAG-CCCC 5690

Sbjct 7248 AAGCCTGACTACGACACACCTGTGGTCCATGGGTGCCCGCTACCACT-CCAGGTCCCC 7306

Query 5691 TCC-GATACCACCTCCACGGAGGAAGAGGAGGTTGTCTGTGAGAATCTACCGTGTCTT 5749

Sbjct 7307 TCCTG-TGCCCTCCGCTCGGAAAAGCGTACGGTGGTCTCACCAGATCAACCTTATCTA 7365

Query 5750 CTGCCCTGGCGGAGCTGCGCAC-AAAGACCTTCGGCAGCTCCG-AATCGTC-GGCGCTCG 5806

Sbjct 7366 CTGCCCTGGCGGAGCTTGCCACCAAA-AGTTTTGGCAGTCTCTCAA-CTTCCGGCATT-- 7421

Query 5807 ACAG-CGGCA---CGGCAACGGCTCTCCTGACAGGCC-TCC-GACGACGGGACGCGG 5860

Sbjct 7422 ACCGGGACAAATACGACAACATCTCTGA-GCCC-GCCCTCTCTG--G-CTGCCCGCCG 7476

Query 5861 GA-TCCGACGTTGAGTCTACTCTCTCCATGAGGGGGAGCGGGGGATCCC 5919

Sbjct 7477 -ACTCCGACGTTGAGTCTATTCTTCCATGCCCGCCCTGGAGGGGAGGCTGGGGATCCG 7535

Query 5920 GATCTCAGCGACGGGTCTTGGTCTACCGTAAGC-GAGGAGGCT-AGT-G-AGGACGTCGT 5975

Sbjct 7536 GATCTCAGCGACGGGTCTAGGTGACGGTCAGTAGTG-GGCCGACACGGAAGATGTGCT 7594

Query 5976 CTGCTGCTCGAGTCTCTACACATGGACAGGCGCCCT-GATCAGCGCATGCGCTGCGGAGG 6034

Sbjct 7595 GTGCTGCTCAATGTCTTATCTCTGGACAGGCGCACTCG-TCACCCCTGCGCTGCGGAGG 7653

Query 6035 AA-ACCAAGCTGCCCATCAATGCACTGAGCAACTCTTTGCTCCGTACCCACAA-CTTGGT 6092

Sbjct 7654 AACAAAAA-CTGCCCATCAACGCACTGAGCAACTCGTGTCTACGCCATCACAATCT-GGT 7711

Query 6093 CTATGCTACAACTATCTCGACGCGAAGCCTGCGGCAGAGAAGGTACACCTTTGACAGACT 6152

Sbjct 7712 GTATTCCACCACTTACGCGAGTGCTTGCCAAAGGACAGAGAAGTTCACATTGACAGACT 7771

Query 6153 CGAGGTCTGGAC-GACCACTACCGGACGTGCTCAAGGAGATGAAGGC-GAAGCGCTCC 6210

Sbjct 7772 GCAAGTCTGGGACAG-CCATTACCAGGACGTGCTCAAGGAGTCAAGGACG-GGCGTCA 7829

Query 6211 ACAGTTAAGGCTAACTT-CTATCCGTGGAGGAAGCTGTAGG-TCAGCCCCCACATT 6268

Sbjct 7830 AAAGTGAGGGCTAA-CTTGCTATCCGTAGAGGAAGCTTGCA-GCCTGACGCCCCACATT 7887

Query 6269 CGGCCAGATCTAAATTTGGCTATGGGGCAAGGACGTCGGGAACCTAT-CCAGCAAGGCC 6327

Sbjct 7888 CAGGCCAAATCCCAAGTTTGGCTATGGGGCAAGGACGTCGGTTGCC-ATGCCAGAAAGGCC 7946

Query 6328 GTTAACCT-ACATCCCGCTCCGTGTGGAAGGAC-TTGCTGGAAGACACATG-AGACACCAATT 6384

Sbjct 7947 GT-AGCCCCACATCAACTCCGTGTGGAAGGACCTT-CTGGAAGACAGTGTA-ACACCAATA 8003

Query 6385 GACACCACCATCATGGCAAAAAATGAGGTTTCTCGCTCCACACGAGAAGGGGGGGCGC 6444

Sbjct 8004 GACACTACCATCATGGCCAAGAACGAGGTTTCTCGCTTACGCTGAGAAGGGGGGTGCT 8063

Query 6445 AAGCCAGCTCGCCTTATCGTATTCACGATTTGGGGGTTTCGTGTGTCGAGAAAAATGGCC 6504

Sbjct 8064 AAGCCAGCTCGCTCATCGTGTTCGCCGACCTGGGCGTGGCGGTGTCGAGAAAGATGGCC 8123

Query 6505 CTTTACGATGTGGTCTC-CACCCCTCCCTCAGGCGGTGATGGGCT-CTTCATACGATTTC 6562

Sbjct 8124 CTGTACGACGCTGGT-TAGCAAGCTCCCCCTGGCGGTGATGGGAAGCTTC-TACGATTTC 8181

Query 6563 AATACTCTCCCTGGACAGCGGTCGATTTCCTGGTG-AATGCCTGGAAA-GAAGAA-AT 6619

Sbjct 8182 AATACTCACCAGGACAGCGGTTGAATTCCTCGTGCA-GCGTGGAA-GTCCAAGAAAGAC 8239

Query 6620 GCCCTATGGGCTTCGCATATGACACCCGCTGTTTGAAGTCAACGGTCACTGAGAATGACA 6679

Sbjct 8240 -CCCGATGGGGTTCCTCGTATGATACCCGCTGTTTGAAGTCCACAGTCACTGAGAGCGACA 8298

Query 6680 TCCGTGTTGAGGAGTCAATCTACCAATGTTGTGACTTGG-CCCCGAAGCCAGACA-GGC 6737

Sbjct 8299 TCCGTACGAGGAGGCAATTTACCAATGTTGTGACTTGGACCTGGACCCCC-AAGCCG-CGTGGC 8356

Query 6738 CAT-AAGGTGCGCTCAGAGCGGCTTTACATCGGGGGCCCCCTGACTAATTTCTAAAGGGC 6796

Sbjct 8357 CATCAAG-TCCCTCAGTACGAGGCTTTATGTTGGGGGCGCTCTTACCAATTC-AAGGGG 8414

Query 6797 -AGAACTGCGGCTATCGCGGTCGCGCGCAGCGGTGATGACGACGAGCTCGGTAAT 6855

Sbjct 8415 GAAAACGCGGCTACGCGAGGTGCGCGCAGCGGCTGATGACAACATAGCTGTGGTAAC 8474

Query 6856 ACCCTCACATGTTACTTTGAAGGCCGCTG-CGGCTGTCGAGCTGCGAAG-CTCCAGGACT 6913

Sbjct 8475 ACCCTCACTTGTGATACAAAGGCC-CGGGACGCTGTCGAGCCG-AGGGCTCCAGGACT 8532

Query 6914 GCACGATGCTCGTATGCGGAGACGACCTT-GTCGTTATCTGTGAAAGCGCGGGGACCCAA 6972

Sbjct 8533 GCACCATGCTCGTGTGTGGCGACGAC-TTAGTCTGTATCTGTGAAAGTGGCGGGTCCAG 8591

Query 6973 GAGGACGAGGCGAGCCT-ACGGGCTTACGAGGCTATGACTAGATACCTCTGCCCCC 7031

Sbjct 8592 GAGGACGCGGCGAGGCTGA-GAGCCTTACGAGGCTATGACCAGGTACTCGCCCCCCCC 8650

Query 7032 TGGGGACCCGCCCA-AACCAGAAATACGACTTGGAG-TTGATAAATCATGCTCCTCCAAT 7089

Sbjct 8651 CGGGGACCC-CCCAACAACAGAAATACGACTTGGAGCTT-ATAAATCATGCTCCTCCAAC 8708

Query 7090 GTGTCAGTCGCGCAGCATG-CATCTGGCAAA-AGGGTGTACTATCTACCCGTGACCCCA 7147

Sbjct 8709 GTGTCAGTCGCGCAGCAGCGC-CTGG-AAAGAGGGTCTACTACCTTACCCGTGACCCTA 8766

Query 7148 CCACCCCTTTCGCGGGGCTGCGTGGGAGACAGCTAGACACATCCAGTCAATTCCTGGC 7207

Sbjct 8767 CAACCCCTTTCGCGAGGCGCGTGGGAGACAGCAAGACACATCCAGTCAATTCCTGGC 8826

Query 7208 TAGGCAACATCATGATGTATGCGGCCAC-CTTGTGGGCAAGGATGATCCTGATGACTAT 7266

Sbjct 8827 TAGGCAACATAATCATGTTTGGCCCCACACT-GTGGGCGAGGATGATACATGATGCCAT 8885

Query 7267 TTCTTCTC-CATCCTTC-TAGCTCAGGAA-CAACTTGA AAAAGCCCT-AGATTGTGAGAT 7322

Sbjct 8886 TTCTT-TAGCGTCT-CATAGC-CAGGGATCAGCTTGAACAGGCTCTTA-ACTGTGAGAT 8941

Query 7323 CTACGGGGCTGTTACTCCATTGAGCCATTGACCTACCTC-AGATCATTCAACGACTCC 7381

Sbjct 8942 CTACGGAGCCTGCTACTCCATAGAACCAGCTGGATCTACCTCCA-ATCATTCAAAGACTCC 9000

Query 7382 ATGGCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTT 7441

Sbjct 9001 ATGGCCTCAGCGCATTTTCACTCCACAGTTACTCTCCAGGTGAAATCAATAGGGTGGCG 9060

Query 7442 CATGCCCTCAGGAACTTGGGGTACCGCCTTGCAGTCTT-GGAGACATCGGGCCAGAAGT 7500

